

10337

10					20					30					40					50					60				
GCC	CAG	GAA	AA <sup>•</sup> C	ACC	TTT	GGG	AAC	AAA	CTC <sup>•</sup>	TTC	CTT	TGA	TGG <sup>•</sup>	AAA	ATG <sup>•</sup>	CAG <sup>•</sup>	AGG	CCC	TTC <sup>•</sup>										
															<u>M O R P F</u>														
70					80					90					100					110					120				
CTC	TCT	GTG	CCG <sup>•</sup>	TGC	TTG	CTC <sup>•</sup>	CTC	TTA	CCT <sup>•</sup>	GCC	CGG	GTG	GTT <sup>•</sup>	TGG	GGG	TGT <sup>•</sup>	TGG	TGT	TTC <sup>•</sup>										
<u>L</u>	<u>S</u>	<u>V</u>	<u>P</u>	<u>C</u>	<u>L</u>	<u>L</u>	<u>L</u>	<u>L</u>	<u>P</u>	<u>A</u>	<u>R</u>	<u>V</u>	<u>V</u>	<u>W</u>	<u>G</u>	<u>C</u>	<u>W</u>	<u>C</u>	<u>F</u>										
130					140					150					160					170					180				
CTC	CCT	GGA	GAA <sup>•</sup>	GAT	GGG	GGA <sup>•</sup>	GGC	TGT	CCC <sup>•</sup>	ACT	CCC	AGC	TCT <sup>•</sup>	GGC	AGA	ATC <sup>•</sup>	AAG	CTG	TTG <sup>•</sup>										
<u>L</u>	<u>P</u>	<u>G</u>	<u>E</u>	<u>D</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>C</u>	<u>P</u>	<u>T</u>	<u>P</u>	<u>S</u>	<u>S</u>	<u>G</u>	<u>R</u>	<u>I</u>	<u>K</u>	<u>L</u>	<u>L</u>										
190					200					210					220					230					240				
CAG	CAG	TGC	CTT <sup>•</sup>	CTT	CAT	CCT <sup>•</sup>	TCC	TTA	CGA <sup>•</sup>	TCA	ATC	ACA	GTC <sup>•</sup>	TCC	AGA	AGA <sup>•</sup>	TCA	GCT	CAA <sup>•</sup>										
<u>Q</u>	<u>Q</u>	<u>C</u>	<u>L</u>	<u>L</u>	<u>H</u>	<u>P</u>	<u>S</u>	<u>L</u>	<u>R</u>	<u>S</u>	<u>I</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>R</u>	<u>R</u>	<u>S</u>	<u>A</u>	<u>Q</u>										
250					260					270					280					290					300				
TTG	CTG	TGC	AGG <sup>•</sup>	TTA	AAA	CTA <sup>•</sup>	CAG	AAC	CAC <sup>•</sup>	ATC	CCA	AAG	GTA <sup>•</sup>	CCT	GGT	AAG <sup>•</sup>	AAT	GTT	TGA <sup>•</sup>										
<u>L</u>	<u>L</u>	<u>C</u>	<u>R</u>	<u>L</u>	<u>K</u>	<u>L</u>	<u>Q</u>	<u>N</u>	<u>H</u>	<u>I</u>	<u>P</u>	<u>K</u>	<u>V</u>	<u>P</u>	<u>G</u>	<u>K</u>	<u>N</u>	<u>V</u>	<u>*</u>										
310					320					330					340					350					360				
AAG	ATC	TTC	CAT <sup>•</sup>	TTC	TAG	GAA <sup>•</sup>	CCC	CAG	TCC <sup>•</sup>	TGC	TTC	TCC	GCA <sup>•</sup>	ATG	GCA	CAT <sup>•</sup>	GCT	TCC	ACT <sup>•</sup>										
370					380					390					400					410					420				
CCA	TCC	ATA	CTG <sup>•</sup>	GCA	TCC	TCA <sup>•</sup>	AAT	AAA	CAG <sup>•</sup>	ATA	TGT	ATA	CAT <sup>•</sup>	AAA	AAA	AAA <sup>•</sup>	AAA	AAA	AAA <sup>•</sup>										

AA

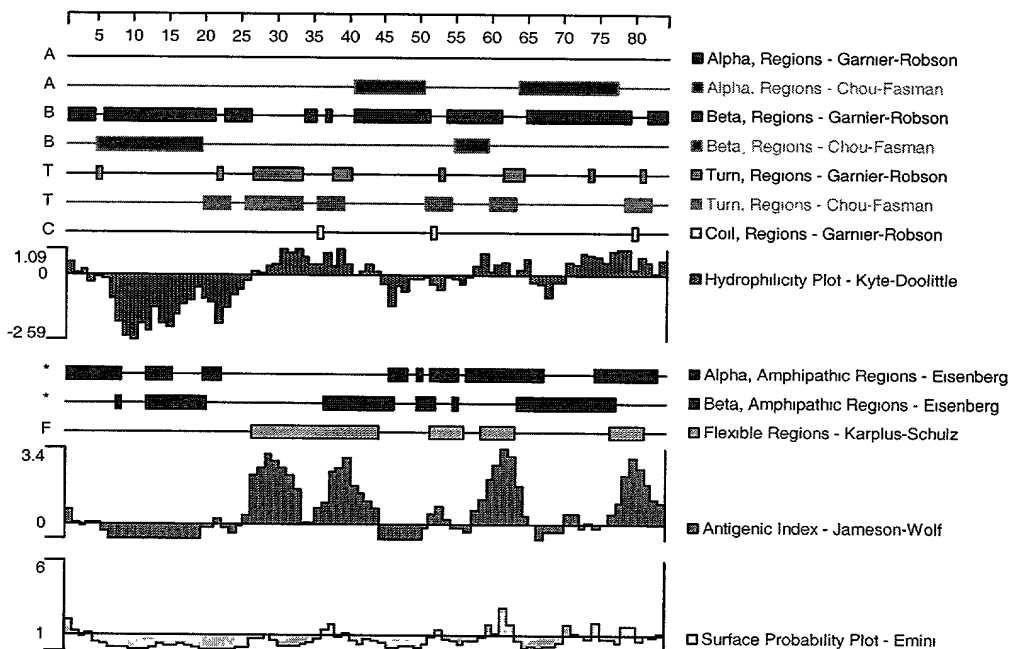
FIG. 2

	C	X	C	X	R	P	G	X	K	-	V	X	X	X	T	I	X	K	L	X	I	K	P	X	Y	P	-	-	Q	C	X	K	X	E	V	I	I	S	L	K	Majority	
	10										20										30										40											
1	C	K	C	S	R	K	G	P	K	-	I	R	Y	S	D	V	K	K	L	E	M	K	P	K	Y	P	-	-	H	C	E	E	K	M	V	I	I	T	T	K	cka-2	
1	C	T	C	L	R	V	T	L	R	-	V	N	P	K	T	I	G	K	L	Q	V	F	P	A	A	P	-	-	Q	C	S	K	V	E	V	V	A	S	L	K	cka-3	
1	C	L	C	I	G	P	G	V	K	A	V	K	V	A	D	I	E	K	A	S	I	-	-	M	V	P	S	N	N	C	D	K	I	E	V	I	I	T	L	K	cka-4	
1	C	W	C	F	L	P	G	E	D	G	G	C	P	T	P	S	S	G	R	I	K	L	L	-	-	-	Q	Q	C	L	L	H	P	S	L	R	S	I	-	cka-6		
	X V S R X X G Q X X C - L X P K X X X X K X X I K X X X X X X E R X - F - - Majority																																									
	50										60										70																					
38	S	V	S	R	Y	R	G	Q	E	H	C	-	L	H	P	K	L	Q	S	T	K	R	F	I	K	W	Y	N	A	W	N	E	K	R	R	F	Y	E	E	cka-2		
38	N	-	-	-	-	-	G	K	Q	V	C	-	L	D	P	E	A	P	F	L	K	K	V	I	Q	K	I	L	D	S	G	T	R	N							cka-3	
39	E	-	-	-	N	K	G	Q	-	R	C	-	L	N	P	K	S	K	Q	A	R	L	I	I	K	-	-	-	K	V	E	R	K	N	F							cka-4
37	T	V	S	R	R	S	A	Q	L	L	C	R	L	K	L	Q	N	H	I	P	K	V	P	G	K	N	V														cka-6	

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

20250720 14:00:00

**FIG 3**



[illegible]

Genbank accession no. gb|AA410918 (SEQ ID NO:6)  
zv39e03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756028

```
1  ggctgtccca ctccagctc tggcagaatc aagctgtgtgc agcagtgcc tttctatcct
61  tccttacgat caatcacagt ctccagaaga tcagctcaat tgctgtgcag gttaaaacta
121 cagaaccaca tcccaaaggt acctggttaag aatgtttgaa agatcttcca tttctaggaa
181 cccagtcctt gtttctccgc aatggcacat gcttccactc catccatact ggcattccta
241 aataaacaga tatgtataca t
```

Genbank accession no. gb|AA411042 (SEQ ID NO:8)  
zv40c03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756100

```
1  tatgtatata tatctgttta tttgaggtat ccagatattgga tgggagtggaa gcatgtgtcca
61  ttgtcggagaa gcaggactgg ggttcctaga aatggaagat ctttcaaacaa ttcttaccag
121 gtaccttttg gatgtggttc tgtagtttta acctgcacag caattgagct gatctttctg
181 agactgtgat tgatcgttaag gaaggatgaa gaaggcactg ctgcaacagc ttgattctgc
241 ca
```

Genbank accession no. gb|AA325795 (SEQ ID NO:10)  
EST28851 Cerebellum II Homo sapiens cDNA 5' end.  
1 agaaccacat cccaaaggtta cctggttaaga ntgtttgaaa gatcttccat ttctaggaac  
61 ccaggtcctg cttctccgca atggcacatg cttccactcc atccatactg gcatictcaa  
121 ataaacagat atgtatacat at

Genbank accession no. gb|D20974 (SEQ ID NO:11)  
 1 gatctcccat ttctaggaac ccagtcctg cttctccgca atggcacatg cttccactcc  
 61 atccatactg gcactctcaa ataaacagat atgtatacat ataaa

**POLYMER LETTERS**

SEQ ID NO:13  
TTATTAGGAGCAAAAGTAATGAGGCCAGGAAACACCTTTGGGAACAAACTCTTCCTTTGATGGAAAA  
TGCAGAGGCCCTTCTCTCTGTGCCGTGCTTGCTCCTCTTACCTGCCCGGGTGGTTTGGGGGTGTTGGT  
GTTTCCTCCCTGGAGAAAGATGGGGGAGGCTGTCCCACTCCCACTGTGGCAGATCAAGCTGTTGCAGC  
AGTGCCCTTCTTCATCCTTCTTACGATCAATCACAGTCTCCAGAGATCAGCTCAATTGCTGTGCAGGT  
TAAAACTACAGAACCACATCCCAAAGGTACCTGGTAAGATGTTTGAAAGATCTTCCATTTCTAGGAAC  
CCCAGTCTGCTTCTCCGCAATGGCACATGCTTCCACTCCATCCATACTGGCATCTCAAATAACAGA  
TATGTATACATAAAAAAAAAAAAAAAAAAACTCGTAG

HCEOU59R (SEQ ID NO:14)  
1 AGAACCACAT CCCAAAGGTA CCTGGTAAGA NTGTTTGAAA GATCTTCCAT TTCTAGGAAC  
61 CCCAGTCCTG CTTCTCCGCA ATGGCACATG CTCCACTCC ATCCATACTG GCATCCTCAA  
121 ATAAACAGAT ATGTATACAT AT